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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9nim2 babesia mic	Q9nim4 babesia mic	Q20227 caenorhabdi	Q12037 saccharomyc	Q9jg50 ttv-like mi	Q927w9 chlamydia p	001439 caenorhabdi	Q56267 thiobacillu	Q928k7 chlamydia p	Q9pm90 campylobact	Q03280 saccharomyc	Q92951 homo sapien	Q9vby9 drosophila	013657 schizosacch	Q9fn33 arabidopsis	Q9qyx6 mus musculu
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                                   Eukaryota: Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
NCBI_TaxID=5868;
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NCBL_TaxID=6239;
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EMBL; Z69302; CAA93261.1; -...
INGERPC: IPRO313439, ABC_LTansportr.
PROSITE: PS00213 ABC_RANSPORTER; UNKNOWN 1.
SEQUENCE 879 AA; 99694 MW; BE4403D836B7E3C2 CRC64;
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                                                                                                                                                            396 AA; 44720 MW; 706E153BA5EE6B7C CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
SEROREACTIVE ANTIGEN BMNI-17 (FRAGMENT).
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Infect. Immun. 68:2783-2790(2000).
EMBL; AF206526; AAF68253.1; -.
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Miosga T., Zimmermann F.K.;
"Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7 kb fragment of chromosome XII including an open reading frame homologous to the human cystic fibrosis transmembrane conductance regulator protein CFTR.";
Yeast 12:693-708(1996).
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STRAIN=FY23 / RROD6 (DERIVED FROM S288C);
STRAIN=FY23 / RROD6 / PUDMed-1986220;
Damak F., Boy-Marcotte E., Le-Roscouet D., Guilbaud R., Jacquet M.;
"SDC25, a CDC25-like gene which contains a RAS-activating domain and is a dispensable gene of Saccharomyces cerevisiae.";
Mol. Cell. Biol. 11:202-212(1991).
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"DNM1, a dynamin-related gene, participates in endosomal trafficking
in yeast.";
J. Cell Biol. 130:553-566(1995).
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STRAIN=FY23 /RD005 (DERIVED FROM S288C);
MEDLINE=94375516; PubMed=8089172;
MEDLINE=94375516; PubMed=8089172;
MEDLINE=94375516; PubMed=8089172;
"MMM1 encodes a mitochondrial outer membrane protein essential for establishing and maintaining the structure of yeast mitochondria.";
                                                   SDC25 OR SCD25 OR L1309/SCD25 OR YLL016W.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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STAIN-FR23 /RD005 (DERIVED FROM S288C);
MEDLINE=93087480; PubMed=1454790;
Ripmaster T.L., Vaughn G.P., Woolford J.L. Jr.;
Ripmaster T.L., Vaughn H.P., Woolford J.L. Jr.;
A putative ATP-dependent RNA helicase involved in Saccharomyces cerevisiae ribosome assembly.";
Proc. Natl. Acad. Sci. U.S.A. 89:11131-11135(1992).
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SEQUENCE FROM N.A.
STRAIN-ALPHA S288C;
Purnelle B., Goffeau A.;
Purnelle B., Goffeau A.;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL PROTEIN L1309.
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STRAIN-FY23 /RD005 (DERIVED FROM S288C);
MEDLINE-95348179; Pubmed-7622557;
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STRAIN-FY23 /RD005 (DERIVED FROM S288C);
MEDLINE-96405918; Pubmed-8810043;
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EMBL; X97560; CAA66161.1; -.
EMBL; 273121; CAA97461.1; -.
EMBL; X91488; CAA6775.1; -.
SGD; SG003939; SDC25.
InterPro; IPR000651; RasGEFN.
InterPro; IPR001895; RasGRF_CDC25.
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Submitted (MAY-1996) to
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STRAIN-INCO265
MEDLINE-20428649; PubMed-10971131;
MEDLINE-20428649; PubMed-10971131;
Takahashi K., Hijikata M., Samokhvalov E.I., Mishiro S.;
"Full or near full length nucleotide sequences of TT virus variants (types Salaban and YouBan) and the TT virus-like mini virus.";
Intervirology 43:119-123 (2000).
EMBL; AB036630; BAA93609 1; -
Intervirology 43:119-123 (2000).
Famp: PPC02956; TT_ORFI:
SEQUENCE 661 AA; 78995 MW; 83CE5F93AlAD286A CRC64;
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                        SMART; SMO0147; RASGEF; 1.
SMART; SM00229; RASGER; 1.
PROSITE; PS00720; GDS_CDC25; 1.
SEQUENCE 1048 AA; 121960 MW; 40AIF12F9B86F458 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mishiro S., Hijikata M., Takahashi K.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
NCBL_TaxID=83558;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILARITY TO CHIPS INCA (CPJ0885 PROTEIN).
CPN0585 OR CPJ0585 OR CPQ163
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                                                                                                                                                                       Query Match 38.8
Best Local Similarity 45.0
Matches 9; Conservative
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Pfam; PF00618; RasGEFN;
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01-OCT-2000 (
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MEDITAR 20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Barry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.
Eisen J., Fraser C.M.;
Peneumoniae AR39.";
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Direct Submission.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: U97016; AAB52352.1;
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SEOUENCE 196 AA; 21516 MW; AFBFFBE84C60EF48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      il protein; Complete proteome.
651 AA; 75668 MW; 7EAC83171535CAB8 CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 21.5 KDA PROTEIN.
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Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                  pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
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STRAIN-BRISTOL N2;
MEDLINE-99069613; Pubmed-9851916;
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STRAIN-BRISTOL N2;
Scheet P., Gattung S.;
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Best Local Similarity
Matches 8; Conserv
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Query Match
Best Local Similarity
Matches 10; Conserv
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                                     Gaps
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Deanne S.M., Rawlings D.E.;
"The gene for the Thiobscillus ferrooxidans ATCC33020 glutamate synthase (GOGAT) small subunit complements an Escherichia coli gltb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                    ;
                                                                                                                                                                                                                                                   Thiobacillus ferrooxidans.
Bacteria; Proteobacteria; gamma subdivision; Acidithiobacillus.
NCBI_TaxID=920;
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           Length 196;
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                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases
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EMBL: U36427: AAA79783.1; -.

EMBL: U36427: AAA79783.1; -.

EMBL: U36427: AAA79783.1; -.

EMBL: U36427: AAA79783.1; -.

InterPro; IPR001359: AABTOR_reductase.

InterPro; IPR001205; NAD_binding.

Pfam; PF00070; PYL redox; 1.

PRINTS; PR00419; AAXPATSE.

FAD; Flavoprotein: Oxidoreductase.

SEQUENCE 465 AA; 50793 MW; B38EAD4B4D0BEE6A CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CTOBS HYPOTHETICAL PROTEIN.
CPN0331 OR CPJ0331 OR CP0426.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) GLUTAMATE SYNTHASE SMALL SUBUNIT GLTD.
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         ore 50; DB 5;
ed. No. 16;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.0%; Score 50; DB 2; 50.0%; Pred. No. 40; ive 2; Mismatches
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         Score 50;
Pred. No.
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MEDLINE=99206606; PubMed=10192388;
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STRAIN-AR39;
MEDLINE-20150255; PubMed-10684935;
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105 KASDKRKKKANKKSPRTQETQEV 127
                                                             2 KPNTNKSEKAERKSHDTQTTQEI 24
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        36.0%;
nilarity 43.5%;
Conservative
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Matches 10; Conservative
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         Query Match
Best Local Similarity
Matches 10; Conserv
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Q9Z8K7
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
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STRAIN-NTC 11168;
MEDLINE-20150912; PubMed-10688204;
MEDLINE-20150912; PubMed-10688204;
MEDLINE-20150912; PubMed-10688204;
Barkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
The genome sequence of the food-borne pathogen Campylobacter jejuni
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Campylobacter.
NCBL_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                        Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).

EMBL, Acolo1617, AAD18480.1; ---
EMBL, AP002204; AAF38269.1; ---
EMBL, AP002504; BAA98541.1; ---
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                                                                                                                                           "Genome seguences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
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Last annotation update)
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PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; UNKNOWN_1.
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50;
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llarity 47.6%; Pred. No. 80;
Conservative 3; Mismatches 8
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Nature 403:65-668(2000).
BMBL, AL139079; CAB73573.1; -.
InterPro; IPR001450; 4Fe45_ferredoxin.
InterPro; IPR001467; Molybdopterin.
InterPro; IPR001370; MurB.
InterPro; IPR001575; Oxid_FAD_bind.
Pfam; PF01565; FAD_binding_4; 1.
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01-OCT-2000 (TrEMBLrel. 15, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last and
PUTATIVE OXIDOREDUCTASE.
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Best Local Similarity
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MEDLINE=98135459; PubMed=9475118;
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomyċota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Utsugi T., Kikuchi Y.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U33050; AAB64910.1;
EMBL; D63905; BAA21482.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dietrich F.S.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jia Y., Cherry J.M.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. (1, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
08035.1P (UBLQUITIN LIGASE).
TOMI OR D8035.1 OR YDR457W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                   PRT; 3268 AA.
                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 KNNINETQTSIKKV--TMTTQELCE 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 2156-3268 FROM N.A.
                                           707 NKSFKPNEKMHDKRSLQEVFE 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
                   6 NKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGD; S0002865; TOM1.
InterPro; IPR000569; HECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00632; HECT; 1.
SMART; SM00119; HECTC; 1.
PROSITE; PS50237; HECT; 1
                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZINC FINGER PROTEIN.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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Matches
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Q92951
                                                                                                                          RESULT 11
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RC SEQUENCE FYON N.A.

RC STRAIN=BERKELEY.

RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Bogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoon C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Bellew R.M., Busu A., Buxendale J., Bayraktaroglu L., Beasley E.M.,

RA Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Godson K.A., Houston R.A., Howland T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Adalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Alalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Mattei B., McIntosh T.C., McLeod M. P., Morbherson D.L.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzry D.M., Nelson D.L.,

RA Mount S.M., Noy M., Wurphy B., Murphy L., Muzry D.M., Nelson D.L.,

RA Mount S.M., Noy M., Wurby B., Murphy L., Muzry D.M., Nelson D.L.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta;
Pterygota, Neoptera, Endopterygota, Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Drew P.D., Gado A.M., Canning R.D., Nagle J.W., Dehejia A.M., Polymeropoulos M.H., Biddison W.E., Jacobson S., Becker K.G.; "C2H5-546: a zinc finger protein differentially expressed in HTLV-1 infected T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.3%; Score 49; DB 4; Length 273; 50.0%; Pred. No. 32; ive 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                           InterPro; IPRO00962; Znf-C2H2.
Pfam; PF00096; zf-C2H2; 7.
PRINTS; PR00048; ZINCFINGER.
SMART; SM00355; ZnF_C2H2; 7.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6.
PROSITE; PS00157; ZINC_FINGER_CAH2_2; 7.
DNA-binding; Maclad-linding; Nuclear protein; Zinc-finger.
SEQUENCE 273 AA; 31029 WW; 91E714RC665C4734 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 NTNKSEKAERKSHDTQTTQE 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
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CG13649.
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Query Match
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Job time
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Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodge T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Smith H.O., Zheng X.H., Zhong F.N., Wyers E.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kushida N., Yamazaki S., Tanaka T., Jinno K., Haikawa Y., Yamazaki J., Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki K., Ogura K., Otsuka R., Kudoh Y., Yanagida M., Machida M., Zhang M.Q.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                        Score 49; DB 5; Length 400;
Pred. No. 47;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.3%; Score 49; DB 3; Length 803; 34.8%; Pred. No. 96; ive 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duesterhoeff A.;

Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AL021766; CAA16907.1; --

EMBL; AL021766; CAA16907.1; --

EMBL; AL021766; CAA16907.1; --

EMBL; PRO04539; BAA21448.1; --

FINE, PRO1444; COTA.

Hypothetical protein.
                                                                                                                                                                                                                                 45117 MW; 71CA68B1D6B50E3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ll protein.
803 AA; 89396 MW; 5E1DB270D9D83572 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE MEMBRANE PROTEIN YOL130W.
P1066 OR SPBC27812.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                     803 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                            EMBL; AE003750; AAF56387.1; - .
F1yBase: FB970039267; CG13649.
InterPro; IPR003889; FYrich_C.
InterPro; IPR003888; FYrich_N.
SWART; SM00542; FYRC; 1.
SWART; SM00541; FYRN; 1.
SEQUENCE 400 AA; 45117 MW; 7
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                                                                                                                                                                                                                                                                                                                                     320 PNRNEEDQATRRSESTSTQAE 340
                                                                                                                                                                                                                                                                                                                    3 PNTNKSEKAERKSHDTQTTQE 23
                                                                                                                                                                                                                                                             35.3%;
                                                                                                                                                                                                                                                                          Best Local Similarity 42.9
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=972 H-;
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Matches
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013657
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150 KPQSNKKHRGRRVKHSPKSTLEV 172

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RESULT 15 Q9FN33

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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
GENOMIC DNA, CHROMSOME 5, TAC CLONE:K19P17.
Arabidopsis thallana (Mouse-ear cress).
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II: Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structural analysis of Arabidopsis thaliana chromosome 5. III.
Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned PI clones.";
DNA Res. 4:401-414(1997).
EMBL: AB007644; BAB10723.1; -.
SEQUENCE 529 AA; 59398 MW; 6A85A27764416EEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98162728; PubMed-9501997;
Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.9%; Score 48.5; DB 10; Length 529; 38.5%; Pred. No. 74; tive 6; Mismatches 9; Indels 1
529 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   completed: October 11, 2002, 20:40:04
ne : 89 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 38.5
Matches 10; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                          NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tabata S.;
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1;

October 11, 2002, 19:21:53 ; Search time 33 Seconds (without alignments) 30.506 Million cell updates/sec GenCore version 5.1.3 Copyright (φ) 1993 - 2002 Compugen Ltd. OM protein - protein search, using sw model Run on:

US-09-794-764-195 139 1 GKPNTNKSEKABRKSHDTQTTQEICE 26 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 segs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	191 sac	P48552 homo sapien	sacch	002626 caenorhabdi	P82873 arabidopsis	Q15651 homo sapien	homo			Q62261 mus musculu				Q50288 mycoplasma	Q05050 saccharomyc	homo	homo	mus แ	P49228 deinococcus	Q25514 manduca sex	Q03328 bluetongue	Q9gum4 mus musculu					Q9pcg5 xylella fas	P09141 photobacter		56	Q9pjg1 chlamydia m	82	P18151 chlamydia t
SUMMARIES	ΩI	MDJ1_YEAST	RI14_HUMAN	SC25_YEAST	AEX3_CAEEL	OM22_ARATH	TRI7_HUMAN	FXY5_HUMAN	VP6_AHSV3	VP6_AHSV6	SPCO_MOUSE	YN34_YEAST	CALM_EUGGR	SGS3_DROYA	YC00_MYCPN	YMS1_YEAST	RBMA_HUMAN	NFH_HUMAN	CENC_MOUSE	RL32_DEIRA	HUNB_MANSE	VP6_BTV1S	SLAM_MOUSE	YJL3_YEAST	YK01_ARCFU	RK32_CYACA	RL32_MYCPN	RL32_XYLFA	LXB1_PHOLE	SNX6_HUMAN	YDLB_SCHPO	Y868_CHLMU	OM6C_CHLTR	OM6D_CHLTR
	DB	Η.	.⊢.	н.	.⊢.	Н.	, 1,	. .	.—	٦.	cd .	. l.	<u>.</u>	Н	Н,	₽4,	٦	-		Н.		٦.	⊶.	٦.	, . .		, - !-	<u></u> ,		<u></u> .	-!-	, . .	-4-	,- 4
	Query Match Length	511	1158	1253	1409	210	120	178	369	369	2363	533	148	263	798	843	929	1020	906	9	327	328	343	1803	178	25	26	63	325	406	406	436	547	547
de	Query	40.3	38.8	38.8	36.0	35.3	33.8	33.8	33.8	33.8	33.8	33.1	32.4	32.4	32.4	32.4	32.4	32.4	32.0	31.7	31.7	31.7	31.7	31.7	31.3	30.9	30.9	30.9	30.9	30.9	30.9	30.9	30.9	30.9
	Score	26	54	54	.20	49	47		47	47	47	46	45	45	45	45	45	45	44.5	44	44	44	44	44	43.5	43	43	43	43	43	43	43	43	43
	Result No.	1	7	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58	30	31	32	33

	Q61909 mus musculu Q06455 homo sapien				
OM6E_CHLTR OM6L_CHLTR	MTG8_MOUSE MTG8_HUMAN TF28_MFT.TA	ML51_HUMAN KIF9_MOUSE	RBMA_RAT VG01_HSVI1	ST31_MOUSE NADD_CAMJE	NANH_CLOPE
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547 547	577 604 673	703	852 862	1018 181	382
30.9	30.9	30.9	30.9	30.9	30.6
4 4 3	4 4 4 8 8 8	4 4	4 4 3	43.5	42.5
34 35	36 37	0.04	41	4 4 6 4	45

ALIGNMENTS

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-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                          SC25_YEAST
P14771;
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                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
SC25_YEAST
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                EMBL;
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Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
A Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
A Park H.-S., Toyoda A., Ishli K., Totoki Y., Chol D.-K., Soeda E.,
A Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
A Shintani A., Kadoh J., Shibuya K., Kawasaki K., Asakawa S.,
A Shintani A., Sasaki T., Naqamine K., Mitsuyama S., Attonarakis S.E.,
Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Blocker H.,
Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
Lehrach H., Reinhardt R., Yaspo M.-L.;
The DNA sequence of human chromosome 21.";
L. Nature 405:31-319(2000).
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cavailles V., Dauvois S., L'Horset F., Lopez G., Hoare S.,
Kushner P.J., Parker M.G.;
"Nuclear factor RIP140 modulates transcriptional activation by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nomo appress, unacao, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Craniata, Hominidae, Homo.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
16-027-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Nuclear factor RIP140 (Nuclear receptor interacting protein 1).
                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                       Score 56; DB 1; Length 511; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                   PROSITE; PS00656; DNAJ_1; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG; 1.
PROSITE; PS0076; DNAJ_2; 1.
Chaperone; Heat shock; Mitochondrion; Repeat; Transit ITRANSIT
                                                                                                                                                                                                                                                                                007343427C66D2B6 CRC64;
                                                                                                                                                                                                                             CXXCXGXG MOTIF.
                                                                                                                                                                                                                                                       CXXCXGXG MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1158 AA
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                                                                                                                                                                                        MDJ1 PROTEIN.
                                                                                                                                                                                                                                                                     CXXCXGXG
                                                                                                                                                                                                       J-DOMAIN
InterPro; IPR003095; DnaJ.
InterPro; IPR002939; DnaJ_C.
InterPro; IPR001305; DnaJ_CXXCXGXG.
InterPro; IPR0010639; DnaJ_N.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00556; DnaJ c. 1.
Pfam; PF00684; DnaJ_CXXCXGXG; 1.
PRINTS; PR00625; DNAJPROTEIN.
SWART; SM00271; DnaJ; 1.
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                                                                                                                                                                                                                                                                                55561 MW;
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                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                      511
127
186
237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             estrogen receptor.";
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                 511 AA;
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SEQUENCE FROM N.A.
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130
230
247
269
285
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P48552;
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16-OCT-2001
                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                      CHAIN
DOMAIN
DOMAIN
REPEAT
REPEAT
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                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Damak F., Boy-Marcotte E., le Roscouet D., Guilbaud R., Jacquet M.; "SDC25, a CDC25-like gene which contains a RAS-activating domain and is a dispensable gene of Saccharomyces cerevisiae."; Mol. Cell. Biol. 11:202-212(1991).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boy-Marcotte E., Damak F., Camonis J., Garreau H., Jacquet M.; "The C-terminal part of a gene partially homologous to CDC 25 guppresses the cdc25-5 mutation in Saccharomyces cerevisiae."; Gene 77:21-30(1989).
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Rey I., Schweighoffer F., Barlat I., Camonis J., Boy-Marcotte
Guilbaud R., Jacquet M., Tocque B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54; DB 1; Length 1158;
Pred. No. 8.9;
3; Mismatches 11; Indels

      Transcription regulation; Nuclear protein.

      CONFLICT
      124
      124
      P -> R (IN REF. 1).

      CONFLICT
      448
      448
      R -> G (IN REF. 1).

      CONFLICT
      721
      726
      NKGKSE -> TKGRVK (IN REF. 1).

      CONFLICT
      1080
      1080
      108
      108

      SEQUENCE
      1158
      AA;
      126941
      MW;
      81FC424968E9A5F6
      CRC64;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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MEDLINE=89306677; PubMed=2545538;
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                                                                                                                                                                                                                AF248484; AAF62185.1; -... AF127577; AAF35255.1; -... AL163207; CAB90396.1; -.. 602490; -..
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SEQUENCE OF 668-1253 FROM N.A.
                                                                                                                                                                                          EMBL; X84373; CAA59108.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.8%;
llarity 46.2%;
Conservative
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SCD25 OR SDC25 OR YLL016W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
OM22_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
       δ
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                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWASS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The COOH-domain of the product of the Saccharomyces cerevisiae SCD25 gene elicits activation of p21-ras proteins in mammalian cells."; Oncogene 6:347-349(1991)
                                                                -i - FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.
-i - MISCELLANEOUS: SUPPRESSES THE CDC25-5 MUTATION IN YEAST (RESTORES CAMP LEVEL) AND HAS SIMILAR FUNCTIONS AS CDC25.
-i - SIMILARITY: CONTAINS' 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guanine-nucleotide releasing factor; Cell cycle; Cell division;
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2DE2C9EC27E3E60D CRC64;
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"aex-3 encodes a novel regulator of presynaptic activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 54; DB 1; Length 1253;
Pred. No. 9.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEX3_CAEEL STANDARD; PRT; 1409 AA. 002626; 027467; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Regulator of presynaptic activity aex-3. AEX-3 OR C02H7.3.
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POLY-ASN.
POLY-ARG.
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SGD; SO003939; SDC25.
InterPro; IPR000651; RasGEFN.
InterPro; IPR001895; RasGRF_CDC25.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 98 SH3.
74 79 POLY-
434 437 POLX-
584 590 DVVVR
1253 AA; 144979 WW; 2
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STRAIN-BRISTOL N2;
MEDLINE-97282461; PubMed-9136770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00720; GDS_CDC25; 1. PROSITE; PS50002; SH3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00617; RasGEF, 1. Pfam; PF00618; RasGEFN; 1. Pfam; PF00018; SH3; 1. SMART; SM00147; RasGEF; 1. SMART; SM00229; RasGEF; 1. SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M26647; AAA16565.1; -.
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Leimbac D., Minx M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OW22_ARATH STANDARD; PRT; 210 AA.
P82873; Q9F276;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Mitochondrial import receptor subunit TOM20-2 (Translocase of outer membrane 20 kDa subunit 2).
TOM20-2 OR ATIG27390 OR F17L21.18.
Arabidopsis thaliana (Mouse-ear cress).
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
MEDLINE-21016719; PubMed=11130712;
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
                                                                                                                                                                     RAB3. MAY
                                                          Medical Library 2.2.7. Toyonaga R.;
"The rab3 GDP/GTP exchange factor homolog AEX-3 has a dual function
"The rab3 GDP/GTP exchange factor homolog AEX-3 has a dual function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Purification and characterization of the preprotein translocase of the outer mitochondrial membrane from Arabidopsis thallana. Identification of multiple forms of TOM20."; Plant Physiol. 125:943-954(2001).
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SEQUENCE FROM N.A., AND SEQUENCE OF 37-48; 105-114 AND 132-147.
STRAIN-CV. COLUMBIA;
PubMed=11161051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Werhahn W., Niemeyer A., Jaensch L., Kruft V., Schmitz U.K.,
                                                                                                                                                           -i- FUNCTION: GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) FOR REGULATE TWO DIFFERENT PATHWAYS FOR NEURAL ACTIVITIES.
-i- SUBUNIT: BINDS TO CAB-1.
-i- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF NEURONS.
-i- SIMILARITY: CONTAINS 1 DENN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50; DB 1; Length 1409;
Pred. No. 38;
7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1409 AA; 157458 MW; 2DDE6395AC963313 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SER-RICH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guanine-nucleotide releasing factor.
DOMAIN 216 364 DENN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3]
INTERACTION WITH CAB-1.
MEDLINE-20428446; Pubmed=10970871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U93842; AAB52421.1; -. EMBL; U49945; AAC47926.1; -. WORTMPEP; CO247.3; CE16806. InterPro; IPRO01194; DENN. Pfam; PF02141; DENN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.0%;
                                                                                                                       in synaptic transmission."
EMBO J. 19:4806-4816(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
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FXY5_HUMAN
           REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Hutter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., Landin-Hooper S., Lee A., Lee J.W., Lenz C.A., Li J.H., Li Y.-P., Militscher J., Miranda W., Nierman W.C., Osborne B.I., Militscher J., Miranda W., Nierman W.C., Osborne B.I., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., Wuterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., Reguence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                         FOR THE RECCGNITION AND TRANSLOCATION OF CYTOSOLICALLY SYNTHESIZED MITOCHONDRIAL PREPROTEINS. TOGETHER WITH TOM22 FUNCTIONS AS THE MITOCHONDRIAL PREPROPER AT THE SURFACE OF THE MITOCHONDRION OUTER MEMBRANE AND FACILITATES THE MOVEMENT OF PREPROTEINS INTO THE TRANSLOCATION PORE.

SUBUNIT: FORMS PART OF MITOCHONDRIAL RECEPTOR COMPLEX.

SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                               Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: THERE ARE FOUR GENES (TOM20-1, TOM20-2, TOM20 TOM20-4) WHICH ENCODE MITOCHONDRIAL IMPORT RECEPTOR SUBUNITS
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16-OCT-2001 (Rel. 40, Last annotation update)
Thyroid receptor interacting protein 7 (TRIP7) (Fragment).
TRIP7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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MISSING (IN REF. 2).
65EA3327249A62E2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 35, Created)
(Rel. 35, Last sequ
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28.0%;
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168
210 AA;
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Q15651;
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01-NOV-1997
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                                                                                                                                                                                                       -:- FUNCTION: INTERACTS, IN VITRO, WITH THE LIGAND BINDING DOMAIN OF
THE THYROID RECEPTOR (TR). TRIP7 REQUIRES THE PRESENCE OF THYROID
HORMONE FOR ITS INTERACTION.
-:- SUBCELLULAR LOCATION: Nuclear.
-:- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
FXYD domain-containing ion transport regulator 5 precursor (HSPC113).
                                                                                                                                                                                                                                                                                                                                                                                           AND PANCREAS.
                                                                           presence or absence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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MEDLINE-95295737; PubMed-7776974;
Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore D.D.;
"Two classes of proteins dependent on either the presence or
"Two thyroid hormone for interaction with the thyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                    MUSCLE AND HEART. LOWER LEVELS FOUND IN LUNG, LIVER AND -!- SIMILARITY: BELONGS TO THE HMG-14/HMG-17 PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB 1; Length 120;
Pred. No. 7.7;
4; Mismatches 11; Indels
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER 1 1 1 SEQUENCE 120 AA; 13016 MW; 2B7A0B9D352BF78F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 AA.
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Pfam; PF01101; HMG14_17; 1.
SMART; SM00527; HMG14_17; 1.
PROSITE; PS00355; HMG14_17; 1.
Nuclear protein; DNA-binding.
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MEDLINE=20499367; Pubmed=11042152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 GKEGTAPSENGETKAEEAQKTESV 115
                                                                                                                                                                          Endocrinol. 9:243-254(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stem/progenitor cells.";
Genome Res. 10:1546-1560(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
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SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L40357; AAA73877.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.8%;
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Pancreas;
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(serotype 6))
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01-NOV-1997
01-NOV-1997
01-MAR-2002
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                                                                                                                                                                                                                                                                            VP6_AHSV6
064913;
                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                      Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenselib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
MSPSGRLCLLTIVGLILPTRGQTLKDTTSSSSADSTIMDIQ
PYTRAPDAVYTELQPTSPTPTWPADETPQPQTQTQQLEGTD
GPLVTDPETHKSTKA -> MQTLSNIPCFCLHGSLLPSTDL
ATLS (IN ISOFORM 2).
        MEDLINE-21240216; PubMed+11342114;
Omasa T., Chen Y.G., Mantalaris A., Wu J.H.D.;
A CDNA from human bone marrow encoding a protein exhibiting homology to the ATP11/PLM/MAT8 family of transmembrane proteins.";
Blochim. Blochbys. Acta 1577:307-307(2001).
-!- SUBCELLULAR LOCATION; Type I membrane protein (Potential).
-!- SIMILARITY: BELONGS 10 THE FXXD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      African horse sickness virus 3 (AHSV-3) (African horse sickness virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                              FXYD DOMAIN-CONTAINING ION TRANSPORT REGULATOR 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Turnbull P.J., Cormack S.B., Huismans H.;
"Characterization of the gene encoding core protein VP6 of two
African horsesickness virus serotypes.";
J. Gen. Virol. 77:1421-1423(1996).
-!- SIMILARITY: BELONGS TO THE REOVIRUSES VP6 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 1; Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                         S -> A (IN DBSNP:1688005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           7429D5A838B75AA1 CRC64;
                                                                                                                                                                                                                          EMBL; AF177940; AGG09301[1]; -.
InterPro; IPR000272; AFP1G1_PLW_MAT8.
Prem: PF003038; ATP1G1_PLW_MAT8; 1.
PROSITE; PS01310; FXYD; 1.
Transmembrane; Signal; Icnic channel; Ion transport;
Allernative splicing; Polymorphism.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (serotype 3)).
Viruses; dsRNA viruses; Reoviridae; Orbivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR_012349.
HT -> SH (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VP6 protein (Minor inner core protein VP6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
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                                                                                                                                                                                                      EMBL; AF161462; AAF29077.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19453 MW;
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178
97
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                                                                                                                                                                                                                                                                                                                                                                                                                                              140
                                                                                                                                                                                                                                                                                                                                     22
146
165
                                                                                                                                                                                                                                                                                                                                                                                                                         32
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Q64909;
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DOMAIN
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Matches
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Characterization of the gene encoding core protein VP6 of two
African horsesickness virus serotypes.";
J. Gen. Virol. 77:1421-1423(1996).
-!- SIMILARITY: BELONGS TO THE REOVIRUSES VP6 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Pred. No. 25;
2; Mismatches 6; Indels
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Pred. No. 25;
2; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dsRNA viruses; Recviridae; Orbivirus.
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15-DEC-1998 (Rel. 37, Last annotation update)
VP6 protein (Minor inner core protein VP6).
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(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                                                EMBL, U19881; AAB17103.1; -
InterPro; IPR001399; Orbi_VP6.
Pfam; PP0156; Orbi_VP6; 1.
Core protein.
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InterPro; IPR001399; Orbi_VP6.
Pfam; PF01516; Orbi_VP6; 1.
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52.9%;
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Best Local Similarity 52.9
Matches 9; Conservative
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR OF 2199-2304.
MEDLINE=97342712; PubMed=9199409;
Nilges M., Macias M.J., O'Donoghue S.I., Oschkinat H.;
Automated NOESY interpretation with ambiguous distance restraints:
the refined NMR solution structure of the pleckstrin homology domain from beta-spectrin.";
J., Mol. Biol. 269:408-422(1997).
Spectrin beta chain, brain 1 (Spectrin, non-erythroid beta chain 1) (Beta-II spectrin) (Fodrin beta chain).
SPTBNI OR SPTB2 OR SPNB2 OR SPNB-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO J. 14:4676-4681(1995).
-!- FUNCTION: FODRIN, WHICH SEEMS TO BE INVOLVED IN SECRETION,
INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS
THUS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE
                                                                                                                                                                                                                                                                                                                                                                                              "Structure of the pleckstrin homology domain from beta-spectrin."; Nature 369:675-677(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECTRIN-LIKE PROTEINS
                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                    ADMINE-9740985; PubMed-8479293; MEDLINE-9740985; PubMed-8479293; Ma Y., Zimmer W.E., Riederer B.M., Goodman S.R.; "The complete amino acid sequence for brain beta spectrin (beta fodrin): relationship to globin sequences."; Brain Res. Mol. Brain Res. 18:87-89(1993).
                                                                                                                                                                                                                                                                                                                                                         Macias M.J., Musacchio A., Ponstingl H., Nilges M., Saraste M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Structure of the binding site for inositol phosphates in a PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hyvoenen M., Macias M.J., Nilges M., Oschkinat H., Saraste M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOSKELETON AT THE MEMBRANE.
SUBUNIT: LIKE ERYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROJ
ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
-!- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
-!- SIMILARITY: CONTAINS 1 PH DOMAIN.
-!- SIMILARITY: CONTAINS 17 SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 2199-2304.
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PDB; 1MPH; 16-JUN-97.
MGD; MG1:98388; Sph2.
InterPro; IPR001589; Actinin_act_bind.
InterPro; IPR001715; Calponin_hom.
                                                                                                                                                                                                                                                                                               [2]
STRUCTURE BY NMR OF 2199-2304.
MEDLINE-94268558; PubMed=8208297;
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Interpro; IPR002017; Spectrin.
Interpro; IPR001605; Spectrin_PH.
Pfam; PF00307; CH; 2.
Pfam; PF00169; PH; 1.
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                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                STRAIN-BALB/C
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                                                                                                                                                                                                                                                                                                                                                                                Oschkinat H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilmanns M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain.";
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STRAIN=S288C / FY1679;
MEDLINE=96132033; pubMed=8553702;
MEDLINE=96132033; pubMed=8553702;
MEDLINE=96132033; pubMed=8553702;
MABULET K.C.T., Urbanus J.H.M., Planta R.J.;
Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying a ribosomal protein gene cluster, the genes encoding a plasma membrane protein and a subunit of replication factor C, and a novel putative serine/threonine protein kinase gene.";
Yeast 11:1303-1310(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                             Cytoskeleton; Membrane; Repeat; Actin-binding; Capping protein;
                                                                                                                                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hypothetical 61.5 kDa protein in CLA4-PUS4 intergenic region.
                                                                                      ACTIN-BINDING (BY SIMILARITY). CH 1.
                                                                                                                                                                                                                                                                                                                                                                                   33.8%; Score 47; DB 1; Length 2363; 37.5%; Pred. No. 1.7e+02;
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NCBI_TaxID=4932;
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SPECTRIN 7.
SPECTRIN 8.
SPECTRIN 9.
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SPECTRIN 16.
SPECTRIN 17.
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SPECTRIN 2.
SPECTRIN 3.
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SPECTRIN 14.
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SMART; SM00150; SPEC; 16.
PROSITE; PS00019; ACTININ.1; 1.
PROSITE; PS00020; ACTININ.2; 1.
PROSITE; PS50021; CH; 2.
PROSITE; PS50003; PH_DOMAIN; 1.
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nes 9; Conserv
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1988
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2363
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                                                                             3D-structure.
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P48565;
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DOMAIN
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REPEAT
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EMBL; U23084; AAC49105.1; -.

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TRANSMEM TRANSMEM

DR KW FT FT FT SQ SQ

TRANSMEM TRANSMEM TRANSMEM

SEQUENCE Query Match

Matches

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263 AA
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                                                                      Salivary glue protein Sgs-3 precursor.
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SEQUENCE FROM N.A.
STRAIN=ATC 29342 / M129;
MEDLINE=97105883;
MEDLINE=97105883;
                                                                                                                                                                                                                                                                     PIR; S01360; S01360.
FlyBase; FBgn0013172; Dyak\Sgs3.
Repeat; Signal.
                             (Rel. 13, Created)
(Rel. 19, Last seq
(Rel. 40, Last ann
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    STANDARD;
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Matches 8; Conserv
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                                                                                                                                                       NCBI_TaxID=7245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herrmann R.;
                             01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae.
                                                       16-OCT-2001
                                          01-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YC00_MYCPN
050288;
  SGS3_DROYA
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                               SIGNAL
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-1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92241300; PubMed=1572365;
Toda H., Yazawa M., Yagi |Y.;
Toda H., Yazawa M., Yagi |Y.;
"Anino acid sequence of calmodulin from Euglena gracilis.";
Eur. J. Biochem. 205:653-660(1992).
-!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS PIR; JK0008; MCEG.
PIR; S21212; S21212.
                                                                                                                                                       33.1%; Score 46; DB 1; Length 533; 35.0%; Pred. No. 49; 1ve 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 1; Length 148;
Pred. No. 18;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Euglenozoa, Euglenida, Euglenales, Euglena.
NCBI_TaxID=3039;
                                                                                                                            9492A18512F399CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82A1E48108638455 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, P02593, ICDM.
InterPro: IPR002048; EF-hand.
InterPro: SP00036; effand; 4.
SMART: SM00054; EFH: 4.
PROSITE; PS00018; EF-HAND; 4.
Calcium-binding; Repeat; Acetylation; Methylation.
                                                                                                                                                                                                                                                                                                                         P11118;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                               148 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHYLATION
METHYLATION.
EF-HAND 1.
EF-HAND 2.
EF-HAND 3.
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                                                                      POTENTIAL.
                                           POTENTIAL
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                                                                                                               POTENTIAL
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  2715/0; Cario S0005238; YNL294C. | S0005238; Transmembrane.
                                                                                                                              ΜW.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16724 MW;
                                                                                                                                                                                                                              376 ESQDASTDRHDTSSNSEVCD 395
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64.3%;
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Best Local Similarity 64.3.
                                                                                                                            61532
                                                                                                                                                                                                                                                                                                               STANDARD;
Z71570; CAA96212.1;
                                                                                                                                                                     Local Similarity 35.0
nes 7; Conservative
                                                       148
199
230
268
301
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67
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140
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74 RKMHDTDTEEEIKE 87
              SGD; S0005238; YNL2940
Hypothetical protein;
TRANSMEM 95 115
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56
93
129
148 AA;
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148
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CA_BIND
SEQUENCE
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STRAIN-Z; SEQUENCE.

MOD_RES MOD_RES CA_BIND

CA_BIND

SGS3_DROYA

RESULT 13

13

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MOD_RES

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                           Drosophila yakuba (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-96177562; PubMed-8604303;
Hilbert H., Himmelreich R., Plagens H., Herrmann R.;
Sequence analysis of 56 kb from the genome of the bacterium
Mycoplasma pneumoniae comprising the dnaA region, the atp operon and cluster of ribosomal protein genes.";
Nucleic Acids Res. 24:628-639(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : - SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                   (1)
SEQUENCE FROM N.A.
MEDLING=88332966; PubMed=3138416;
Martin C.H., Mayeda C.A., Meyerowitz E.M.;
Martin c.H., Mayeda C.A., Meyerowitz E.M.;
"Evolution and expression of the Sgs-3 glue gene of Drosophila.";
"Fvolution and expression of the Sgs-3 glue gene of Drosophila.";
"Mol. Biol. 201:273-287(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                   24 263 SALIVARY GLUE PROTEIN SGS-3.
263 AA; 28392 MW; C0C5246B482A261C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical lipoprotein MPN200 precursor (GT9_orf798).
MPN200 OR MP631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Potential).
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Pred. No. 32;
6; Mismatches
Last sequence update)
Last annotation update)
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hypothetical 93.3 kDa protein in TAP42-CYK2 intergenic region.
YMR031C OR YM9973.04C.
                                                                                                                                                     POTENTIAL.
HYPOPHETICAL LIPOPROTEIN MPN200.
N-ACYL DIGLYCERIDE (POTENTIAL).
3 52471D7EE0A3CAO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.4%; Score 45; DB 1; Length 843; 56.2%; Pred. No. 1.10+02; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                       32.4%; Score 45; DB 1; Length 798; 40.9%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: TO YEAST YKL050C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 843 AA; 93345 MW; 0068D65A229B941D CRC64;
                                                                                EMBL; U34795; AAC43681.1; -.
EMBL; AE000060; AAB96279.1; -.
Hypothetical protein; Lipoprotein; Membrane; Signal; Complete protecome.

1 22 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                            843 AA.
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798 H3
23 N-
87628 MW;
                                                                                                                                                                                                                                                                                                          2 KPNTNKSEKAERKSHDTQTTQE 23
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                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                      798 AA;
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Matches 9; Conserv
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
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01-NOV-1997
30-MAY-2000
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Q05050;
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YMS1_YEAST
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Search completed: October 11, 2002, 20:38:24 Job time : 35 secs

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; Search time 48 Seconds
(without alignments)
52.048 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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139
1 GKPNTNKSEKAËRKSHDTQTTQEICE 26
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                      OM protein
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

	Description	hypothetical prote	heat shock protein	SCD25 protein (ver	SCD25 protein (ver			hypothetical prote	glutamate synthase	hypothetical prote	conserved hypothet	CT082 hypothetical	probable oxidoredu	presynaptic activi	hypothetical prote		GTP pyrophosphokin	probable hemolysin	probable RNA helic					hypothetical prote	ᇽ	hypothetical prote			probable membrane	hypothetical prote
SUMMARIES	ID	T22033	838898	S64758	S14177	F86563	A72060	T25445	JC5184	AD2545	D72092	C86532	G81253	T37188	869625	T40036	E69844	F71374	A86444	F71621	109076	T45622	G81292	F96831	T10457	T28053	T23785	н90266	S63270	T25572
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	ery ich	3.5	0.3	8.8	3.8	5.7	•	0.9	0.0	0.0	0.0	0.0	0.0	0.5	9.0	ب	7.	8.8	8.8	3.8	8.8	æ.	.5	٠. ت	∵.		3.1			3.1
æ	Query Match	4	4	ñ	ñ	ñ	ĕ	ĕ	ñ	ĕ	ñ	ř	ĕ	ĕ	ĕ	m	ň	m	m	m	m	m	m	m	'n	m	m	m	č	m
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	Result No.	7	7	m	4	ഗ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Cypecies: Saccharomyces creatistic for the control of the control

heat shock protein MDJ1 precursor - yeast (Saccharomyces cerevisiae) N; Alternate names: MDJ1 protein; protein YFL016c

RESULT 2

hypothetical protein F40F8.5 - Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T22033 R;MacDougall, R. submitted to the EMBL Data Library, February 1996 A;Reference number: Z19505 A;Reference number: Z19505	
A:Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: DNA A:Molecule type: DNA A:Molecule type: DNA A:Residues: 1-879 <wil> A:Cross-references: EMBL:Z69302; PIDN:CAA93261.1; GSPDB:GN00020; CESP:F40F8.5 A:Rescinental source: clone F40F8 C:Genetics: A:Genetics: A:Genet</wil>	27 13
Query Match Query Matches 12; Conservative 5; Mismatches 5; Indels 1; Gaps 1;	
Qy 5 TNKSEK-AERKSHDTQTTQEICE 26 : : : : Db 3 TNKREKQLERECHEQKTSQAVCE 25	

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A; Reference number: S70557; MUID:96405918
A; Accession: S70559
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1048 < MIW>
A; Cross-references: EMBL: X91488; NID:91495203; PIDN: CAA62775.1; PID:91495207
A; Octobe: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A; Genetics:
A; Genetics:
A; Genetics: SGD:SCD25; SDC25
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A.Residues: 1-737, A.738-970, T', 972-1250 <DAM2>
A.Cross-references: EMBL:M26647
A. Note: the authors translated the codon GAG for residue 538 as Asp, GTC for residue
A.Note: the authors translated the codon GAG for residue 538 as Asp, GTC for residue
Gene 77, 21-30, 1989
A.Title: The C-terminal part of a gene partially homologous to CDC25 gene suppresses
A.Reference number: PS0040
A.Title: The C-terminal part of a gene partially homologous to CDC25 gene suppresses
A.Reference number: PS0040
A.Residues: 668-679, NPVMTILMC, 689, NV, 691-1250 <BOV>
A.Residues: 668-679, NPVMTILMC, 689, NV, 691-1250 <BOV
A.Residues: 668-679, NPVMTILMC, 689, NV, 691-1250 <BOV
A.Residues: 668-679, NPVMTILMC, NPVMTILMC, NPVMTILMC, NPVMTILMC, NPVMTILMC, NPVMTILMC, NPVMTILMC, NPVMTILMC, NPVMTILMC, NPVMTILMC
                                               R;Miosga, T.; Zimmermann, F.K.
Yeast 12, 693-708, 1996
A;Title: Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7
e conductance regulator protein CFTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: SGD:S0003939; MIPS:YLL016w
Aymap position: 12L
C;Superfamily: CDC25-type guanine nucleotide exchange activator homology
F;946-1197/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>
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A; Residues: 1-1250 < CDAMI>
A; Cross-references: EMBL: M26647
R; Damak, F.; Boy-Marcotte, E.; Le-Roscouet, D.; Guilbaud, R.; Jacquet, M.
Mol. Cell. Biol. 11, 202-212, 1991
A; Title: SDC25, a CDC25-1ike gene, which contains a RAS-activating domain and
A; Reference number: S12942; MUID:91094833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Saccharomyces cerevisiae
C;Date: 02-Jun-1994 # sequence_revision 02-Jun-1994 #text_change 06-Feb-1998
C;Accession: S14177; S12942; PS0040
R;Damak, F.; Boy-Marcotte, E.; Le-Roscouet, D.; Guilbaud, R.; Jacquet, M.
submitted to the EMBL Data Library, August 1989
A;Reference number: S14177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Map position: 12L C:Superfamily: CDC25-type guanine nucleotide exchange activator homology F;744-995/Domain: CDC25-type guanine nucleotide exchange activator homology
        A; Cross-references: EMBL: X97560; NID: 91297003; PID: e238680; PID: 91297014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 54; DB 2;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCD25 protein (version 1) - yeast (Saccharomyces N.Alternate names: protein L1309; protein YLL016w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54; DB;
Pred. No. 14;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: SGD:S0003939; MIPS:YLL016w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1002 PNSNSNNKSQEKSRDDQTDE 1021
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45.0%;
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Best Local Similarity 45.0
Matches 9; Conservative
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                                                                                                                                                                                                                               A;Cross-references: GB:Z28336; NID:9431909; PIDN:CAA82189.1; PID:9431910
R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu Bubnitted to the EMBL Data Library, May 1995
A;Bescription: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces of A;Reference number: S56186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Molecule type: DNA
A.Residues: 1-511 cMUR>
A.Residues: 1-511 cMUR>
A.CLOSS-INEFERENCES: EMBL:D50617; NID:g836685; PIDN:BAA09222.1; PID:g836738; MIPS:YFL016c
R; Murakami, Y
Submitted to the EMBL Data Library, December 1994
A.Reference number: 562230
A.Accession: S62297
                                          DnaJ family, is involved in mitochondrial bioge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Genome: nuclear
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Superfamily: heat shock; membrane protein; mitochondrial inner membrane; mitochondrion;
C;Reywords: heat shock; membrane protein; mitochondrial inner membrane; mitochondrion;
F;1-55-511/Product: peptide (mitochondrian) #status predicted <NAT>
F;61-125/Domain: dnaJ amino-terminal homology <DNJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-1048 A; Residues: 1-1048 A; Cops
A; Estatues: 1-1048 Cops
A; Cross-references: EMBL:Z73121; NID:g1360186; PID:e245452; PID:g1360187; MIPS:YLLO16w
A; Experimental source: strain s288C
R; Purnelle, B.; Goffeau, A
submitted to the EMBL Data Library, April 1996
A; Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals 14
mily and a new ABC transporter homologous to the human multidrug resistance protein.
A; Reference number: S69380
A; Recession: S69390
A; Molecule type: DNA
A; Residues: 1-1048 <PUR>
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A; Residues: 1-1048 <a href="Millor and register">MILLOR A; Residues: 1-1048 <a href="Millor and register">MILLOR CALLOR A; Cross references: EMBL: 273121; NID: 91360186; PID: 9245452; PID: 91360187; MIPS: YLLO16w
A; Experimental source: strain $2288C
R; Goffeau, A.; Purnelle, B.
Submitted to the Protein Sequence Database, May 1996
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A.Residues: 1-511 <MUN>
A.Cross-references: EMBL:D44596; NID:g1100783; PIDN:BAA08001.1; PID:g1100788
G.Genetics:
A.Gene: SGD:MDJ1
A.Cross-references: SGD:S0001878; MIPS:YFL016c
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C;Bate: 01-May-1996 #text_change 21-Jul-2000
C;Bate: 01-May-1995 #sequence_revision 24-May-1996 #text_change 21-Jul-2000
C;Accession: S64758; S64764; S69390; S70559
R;Miosga, T.; Zimmermann, F.K.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64743
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3.6;
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Pred. No.
        A; Reference number: A53500; MUID:94221642 A; Accession: A53500
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Best Local Similarity 50.00
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Cell 77, 249-259, 1994
A; Title: Mdjlp, a novel
                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-511 <RO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S56238
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A Reference number: 220036
A) Accession: T28445
A) Accession: T2845
A) 
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                   C; Accession: T25445
R;Scheet, P:; Gattung, S.
submitted to the EMBL Data Library, April 1997
A; Description: The sequence of C. elegans cosmid B0261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50; DB 2
Pred. No. 9.9;
5; Mismatches
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50.0%; Pre
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43.5%;
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Best Local Similarity
Matches 10; Conserv
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Matches 10; Conser
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence|revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: A7260; B81607
R;Kalman, S:; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1959
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A7200; MUID:99206606
A;Accession: A7206
A;Reference: GB:AE00164; GB:AE001363; NID:94376876; PIDN:AAD18724.1; PID:9437687
A;Residues: 1-651 cARN
A;Residues: 1-651 cARN
A;Cross-references: GB:AE00164; GB:AE001363; NID:94376876; PIDN:AAD18724.1; PID:9437687
A;Experimental source: strain CWL029
B;Read, T.D.; Brunham, R.C.; Ghill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Doddson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-651 cREA
A;Gene: CPR0585; CP0163
                                                                                                                                                                                                                                                                                                                                                                                                             H.
                                                                                                                                                                               hypothetical protein CPj0585 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_Irevision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: F86563
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A;Reference number: A86491; MUID:20330349
A;Reference number: A86491; MUID:20330349
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-651 <STO>
A;Residues: 1-651 <STO>
A;Cenetics:
A;Genetics:
A;Genetics
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Pred. No. 24;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
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Pred. No.
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Similarity 38.18;
8; Conservative
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38.18;
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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R; Deane, S.M.; Rawlings, D.E.
Gene 177, 261-263, 1996
A; Title: Cloning and sequencing of the gene for the Thiobacillus ferrooxidans ATCC330
A; Accession: JC5184; MUID:97080532
A; Accession: JC5184
A; Residues: preliminary; nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 1-465 < DEA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Gene: gltD
C;Superfamily: glutamate synthase small chain
C;Supervords: iron-sulfur protein; metalloprotein; oxidoreductase
C;Keywords: iron-sulfur protein-rich
F;151-156,291-296/Region: glycine-rich
F;427-437/Region: FAD-binding %status predicted
F;45,48,53,57,92,96,102,106/Binding site: iron-sulfur clusters (Cys) (covalent) #stat
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein alr7647 [imported] - Anabaena sp. (strain PCC 7120) plasmid pCC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Anabaena sp. A;Note: Anabaena sp. A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C.Accession: AD2545
glutamate synthase (GOGAT) (EC 1.4.1.-) small chain - Thiobacillus ferrooxidans C;Species: Thiobacillus ferrooxidans C;Date: 16-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 29-Sep-1999 C;Accession: JC5184
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Pred. No. 23;
2; Mismatches 8
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A;Status: preliminary

hypothetical protein B0261.5 - Caenorhabditis elegans C; Species: Caenorhabditis elegans

RESULT 7

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Gaps

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Indels

Length 579

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probable oxidoreductase Cj1585c [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Species: Campylobacter, C;Spabma, D;Chil
C;W:;Quall, M:;Rajandream, M.A.; Retley, J.M.; Churcher, C;Basham, D.; Chil
C;W:;Quall, M:;Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S;Ba
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
A;Reference number: A81250; MUID:20150912
A;Scatus: preliminary
A;Residues: DNA
A;Residues: DNA
A;Residues: 1-923 <PAR>A;Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73573.1; PID:g696
C;Genetics:
A;Gene: Cj1585c
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A;Introns: 77/1; 136/2; 183/2; 232/3; 283/3; 386/3; 427/3; 527/3; 577/1; 699/3; 782/2
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T37188
R;Leimbac, D.; Minx, M.
Submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid C02H7.
A;Reference number: Z20523
A;Accession: T37188
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1409 <LEI>
A;Cross references: EMBL:U49945; PIDN:AAC47926.1; GSPDB:GN00029
A;Experimental source: strain Bristol N2; clone C02H7
A;Genetics:
A;Genetics:
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                                                                                                         DB 2;
29;
                                                                                                                                                                              10; Mismatches
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                                                                                                             Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                   287 GIPNSNTLERAEKEAEKQESREQLSE 312
                                                                                                                                                                                                                                                      1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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                                                                                                      36.0%;
30.8%;
                                                                                                                                                                                     Conservative
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Best Local Similarity 47.6
Matches 10; Conservative
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Best Local Similarity
Matches 8; Conserva
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Matches 8; Conserv
                                     A; Gene: CP; 0331
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       C; Genetics
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S69625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conserved hypothetical protein CP0426 [imported] - Chlamydophila pneumoniae (strains CWI N;Alternate names: ct082 hypothetical protein C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C;Accession: D72092; B81577 R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Astrie Genet. 21, 385-389, 1999 A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Status: preliminary
A Molecule type: DNA
A Molecule type: Molecule 
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A.Molecule type: DNA
A.Residues: 1-579 <REA>
A.Cross-references: GB:AE002204; GB:AE002161; NID:g7189350; PIDN:AAF38269.1; PID:g718935
C.Genetics:
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CT082 chamydophila pneumoniae, Chlamydophila pneumoniae
C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C; Accession: C86532
R; Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I Nucleic Acids Res. 28, 2311-2314, 2000
A; Tille: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A; Reference number: A86491; MUID:20330349
A; Accession: C86532
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-579 cSTO>
A; Cross-references: GB:BA000008; NID:98978705; PIDN:BAA98541.1; GSPDB:GN00142
C*A; Experimental source: strain J138
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                                             A;Cross-references: GB:AP003602; PIDN:BAB77290.1; PID:g17134732; GSPDB:GN00181 A;Experimental source: strain PCC 7120 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                           Length 471;
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                                                                                                                                                                                                                                                                                        DB 2;
24;
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29;
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30.8%; Pred. No. 29;
iive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Pred. No.
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ilarity 45.5%;
Conservative
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Matches 8; Conserv
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Best Local Similarity
Matches 10; Conserv
                              A; Residues: 1-471 <KUR>
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A; Molecule type: DNA
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A; Status: prelimina:
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                                                                                                                                                                              A;Gene: alr7647
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Gaps

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8; Indels

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Gaps

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hypothetical protein YDR457w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S69625
R;Dietrich, F.S.
R
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C; Dete: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C; Decession: T40036
R; Wood, V; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A. Submitted to the EMBL Data Library, December 1997
A; Recession: T40036
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-803 < MOO>
A; Cross-references: EMBL:AL021766; PIDN:CAA16907.1; GSPDB:GN00067; SPDB:SPBC27B12.12c
A; Experimental source: strain 972h-; cosmid c27B12
A; Map position: 2
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Pred. No. 1.6e+02;
6; Mismatches 6; Indels
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Pred. No. 56;
5; Mismatches 10; Indels
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A;Map position: 4R
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44.0%;
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Best Local Similarity 44.0
Matches 11; Conservative
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Best Local Similarity 34.8
Matches 8; Conservative
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Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139
1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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Listing first | 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Human secreted pro
Human channel-rela
Human transmembran
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Human polypeptide
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Human secreted pro Human polypeptide

AAB34321 AAM39757 AAB25692 AAY1674

AAY13945 AAU29294 AAM38819

Drosophila melanog Drosophila melanog

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AAW88709 AAB25703 AAB25704 AAB25705 AAB25705

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Amino acid sequenc Chlamydia pneumoni

Thyroid hormone re Thyroid hormone re Human TR-interacti Human channel-rela

protei

Human polypeptide Mouse elf-3 protei

AAW92388 ABB12045 AAM40605

AAW81640 AAB25706 AAB18176

ABB50476 AAY40581 AAW85100

Human secreted pro Plasmodium falcipa

Mouse elf protein.

Human secreted pro Partial amino acid

ALIGNMENTS

RESULT 1

Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis. Sleath PR; Babesia microti BMNI-20 antigen sequence. ¥ Reed SG, AAW56303 standard; Protein; 275 97US-0845258 96US-0723142 97EP-0117067 Houghton R, Lodes MJ, WPI; 1998-195465/18. N-PSDB; AAV22749. (CORI-) CORIXA CORP Babesia microti 24-APR-1997; 01-OCT-1996; 01-OCT-1997; 28-SEP-1998 EP834567-A2 38-APR-1998 AAW56303; AAW56303

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analys, of the total score distribution.

SUMMARIES

/SIDS1/gcjdata/geneseq/geneseqp-emb1/AA1997.DAT:*/SIDS1/gcjdata/geneseq/geneseqp-emb1/AA1998.DAT:*/SIDS1/gcjdata/geneseqp-emb1/AA1999.DAT:*/SIDS1/gcjdata/geneseq/geneseqp-emb1/AA2000.DAT:*/SIDS1/gcjdata/geneseq/geneseqp-emb1/AA2001.DAT:*/SIDS1/gcjdata/geneseq/geneseqp-emb1/AA2001.DAT:*

111: 123: 123: 117: 120: 220: 221:

Babesia microti BM
Babesia microti an
B. microti clone a
Babesia microti BM
Babesia microti BM
B. microti MN-10/B
B. microti MN-10/B
B. microti MN-10/B
Babesia microti an
B. microti BM-10/B
Human colon cancer

AAW56303 AAY24365 AAB30217 AAW56298 AAY24358 AAB30207 AAB30231 AAB30231 AAB30231 AAB30231 AAB30208 AAB30208

275 275 275 244 445 445 445 1132 32 32 600

100.0 100.0 100.0 100.0 100.0 100.0 100.0 45.3 45.3

139 139 139 139 139 63 63 63

2 3 7 10 10 11

Description

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DB Length

Query Match 1

Score

Result Š. ö

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The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                          Gaps
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               Length 275;
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                                                                                                                                                                                                                                                                                      parasite; tick-borne illness; antigen; disease prevention.
                                          Indels
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             Score 139; DB 20;
Pred. No. 3.4e-13;
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             100.0%; Score 139; Ilarity 100.0%; Pred. No. 3.4 Conservative 0; Mismatches
                                                                                                                                                                                                                                                           B. microti clone antigen SEQ ID NO: 53.
                                                                                     218 GKPNTNKSEKAERKSHDTQTTQEICE 243
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                                                                     1 GKPNTNKSEKAERKSHDTQTTQEICE
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17-MAR-2000; 2000US-0528784.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-686939/67
                                                                                                                                                                                                                                                                                     Babesiosis; rodent
disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 26; Conserv
                           Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                                                  Babesia microti.
                                                                                                                                                                                                                                                                                                                                                             WO200060090-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Babesia microti antigen BMNI-20 complementary open reading frame protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes isolated polypeptides comprising specific immunogenic portions of Babesia microti. AAX88934 to AAX8994 encode specifically claimed B. microti immunogenic proteins, and AAX24327 to AAY24338 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B microti infections.
                                                                                                                                                                                                                                                                                                       Gaps
                                                                one addition to portion of a Babbesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection by detecting specific antibodies of primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick-borne diseases (Lyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
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                                                                                                                                                                                                                                                                          Length 275;
                                                       sequence is that of a polypeptide comprising at least
                                                                                                                                                                                                                                                                                                     Indels
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100.0%; Pred. No. 3.4e-13;
ive 0; Mismatches 0;
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                            Page 101-102; 113pp; English.
infection and in protective vaccines
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                                                                                                                                                                                                                                                                                                                                                AAY24365 standard; Protein; 275 AA.
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N-PSDB; AAX90017.
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Matches 26; Conserv
                                                                                                                                                                                                                                              275 AA;
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Sleath PR;
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The present invention describes isolated polypeptides comprising specific immunogenic portions of Babesia microti. AAX88994 AAX88994 encode specifically claimed B. microti immunogenic proteins, and AAY24327 to AAY24338 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. The present sequence encodes a B.microti antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
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100.0%; Pred. No. 5.9e-13;
live 0; Mismatches 0;
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                                                                                                                                                                                                                                         New isolated Babesia microti polypeptides
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Best Local Similarity 100.(
                                                                                                                             Houghton R,
                                                                                          (MAYO-) MAYO FOUNDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reed SG, Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-686939/67
                                                                         (CORI-) CORIXA CORP
                                                                                                                                                                                 WPI; 1999-385612/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 AA;
                                                                                                                                                                                                    N-PSDB; AAX90012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200060090-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-1999;
11-DEC-1998;
                                    11-DEC-1997;
                                                                                                                             Bruinsma E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2000
                                                                                                                                                Sleath PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB30207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Babesia microti antigen BMNI-17 complementary open reading frame protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is that of a polypeptide comprising at least one antigenic portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using:
(a) primers or probes derived from the coding sequence, in standard amplification of hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick borne diseases (Lyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                  vaccine; tick-borne disease; ehrlichiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
Babesia microti BMNI-17 complement antigen sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 139; DB 19;
Pred. No. 5.9e-13;
                                                                                                                                                                                                                                                                                                                                   Sleath PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection and in protective vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 77-79; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 GKPNTNKSEKAERKSHDTQTTQEICE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY24358 standard; Protein; 445 AA
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                                                                                                                                                                                                                                                                                                                               Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                  antigen; detection; diagnosis;
differentiation; Lyme disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
100.0%;
                                                                                                                                                                                                    97EP-0117067
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96US-0723142
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                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-195465/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunity; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    445 AA;
                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV22753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Babesia microti
                                                                                        Babesia microti
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                                                                                                                                                                                                  01-OCT-1997;
                                                                                                                                                                                                                                                          01-OCT-1996;
                                                                                                                                                                                                                                                                                                                                 Houghton R,
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Sednence

Query Match Matches

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Gaps

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12-FEB-2001
                                                                                                                                                                                                              12-OCT-2000.
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                                                                                                                                                         Babesia sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                       AAB30231;
                                                                                                                                                                                                                                                                                                               Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY24359;
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                         AAB3023
             RESULT
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The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and DNAs encoding the polypeptides, useful for diagnosing, or preventing B. microti infection, or for inducing protective in a patient
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptides containing an antigenic portion of Babesia microti
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                                                                                                 Length 445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McNeill PD;
                                                                                                                                                                                                                                                                                                             parasite; tick-borne illness; antigen; disease prevention.
                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                          85.
                                                                                                                                                                                                                                                                                        B. microti MN-10/BMNI-17 fusion protein SEQ ID NO:
                                                                                                 100.0%; Score 139; DB 21;
llarity 100.0%; Pred. No. 5.9e-13;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 139; DB 21;
ilarity 100.0%; Pred. No. 9.4e-13;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; Page 108-111; 118pp; English.
                                                      prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prevention and treatment of babesiosis
                                                                                                                                                       182 GKPNTNKSEKAERKSHDTQTTQEICE 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houghton RL,
                                                                                                                                            GKPNTNKSEKAERKSHDTQTTQEICE
                                                                                                                                                                                                                       AAB30230 standard; Protein; 666
                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-1999; 99US-0286488.
17-MAR-2000; 2000US-0528784.
                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2000; 2000WO-US09136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-686939/67
                                                                                                                                                                                                                                                                                                               Babesiosis; rodent
                                                                                                                                                                                                                                                                                                                          disease diagnosis;
                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                            445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       666 AA;
                                                                                                                                                                                                                                                                                                                                                                             WO200060090-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating or immunity in
                                                                                                           Local Sim
                                                                                                                                                                                                                                                                                                                                             Babesia sp
                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                              AAB30230;
                                                                             Sequence
                                                                                                  Query Match
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                                                                                                                        Matches
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Matches
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The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                               87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1132;
                                                                                                                             B. microti MN-10/BMNI-17/BMNI-15 fusion protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Babesia microti antigen BMNI-17 degenerate repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McNeill PD;
                                                                                                                                                                      Babesiosis; rodent parasite; tick-borne illness; antigen; disease diagnosis; disease prevention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 139; DB 21;
Pred. No. 1.7e-12;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 7; Page 112-116; 118pp; English.
AAB30231 standard; Protein; 1132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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100.0%;
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17-MAR-2000; 2000US-0528784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY24359 standard; peptide;
                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunity; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-686939/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Babesia microti
                                                                                                                                                                                                                                                                                                          WO200060090-A1.
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The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                        New polypeptides containing an antigenic portion of Babesia microti antition and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient

    microti BMNI-17 antigen reverse complement repeat SEQ ID NO: 39.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 63; DB 21; Length 32;
Pred. No. 0.013;
                                                                            parasite; tick-borne illness; antigen; disease prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human colon cancer antigen protein SEQ ID NO:5856.
                                                                                                                                                                                                                                                                                                      Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colorectal carcinoma; chromosome 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG75092 standard; Protein; 600 AA.
                                                                                                                                                                                                                                                                                                      Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 88; 118pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.3%;
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17-MAR-2000; 2000US-0528784.
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                               (first entry)
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                                                                                                                                                                                                                                                                                                      Lodes MJ,
                                                                                                                                                                                                                                                                                                                              WPI; 2000-686939/67.
                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                    rodent
                                                                                                 disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 AA;
                                                                                                                           Babesia microti
                                                                                                                                                   WO200060090-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-SEP-2001
                             12-FEB-2001
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                                                                                   Babesiosis;
                                                                                                                                                                               12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG75092;
    AAB30208;
                                                                                                                                                                                                                                                                                                    Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes isolated polypeptides comprising specific immunogenic portions of Babesia microti. AAX88933 to AAX88994 encode specifically claimed B. microti immunogenic proteins, and AAX24337 to AAX24338 représent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They microti infections. The present sequence represents a B.microti antigen BMNI-17 degenerate repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Persing D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 63; DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.013;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Babesia microti polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
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                                                                                                                                                                                                        Tyr
                                                                                                                                                                                                                                  Pro
                                                                                                                                                                                                                                                             Thr
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m Glu}
                                                                                                                                                                                                                                                                                                                                            Ala
                Gly, Asp
                                                                   Thr
                                                                                             G1y
                                                                                                                                                   G1y
                                                                                                                                                                                                                                                                                                                                                                     /label= Cys, His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KPNTNKSEKAERKSHDTQTTQE 23
                                                                                                                           Ľys,
                                                                                                                                                                               ile,
                                           Pro,
                                                                                                                                                                                                          His,
                                                                                                                                                                                                                                                                                                                                          'label= Glu,
                                                                                              label= Glu,
                                                                                                                                                    label= Glu,
                                                                                                                                                                                                                                                                                       'label= Cys,
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63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 KXNXNKSXXAXXKSXDTQTXQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US26437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0990571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 94; 126pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                       /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-385612/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 14; Conserv
Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 AA;
                                                    Misc-difference
                                                                                                           Misc-difference
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WO9929869-A1

17-JUN-1999.

11-DEC-1998; 11-DEC-1997;

3ruinsma E, Sleath PR;

McNeill PD;

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Gaps

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8; Indels

28-SEP-2000; 2000WO-US26524.

99US-0157137

29-SEP-1999;

AAB30208 standard; Peptide; 32 AA

RESULT 10 AAB30208 ID AAB3

QQ

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Sequence

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The specification describes a crystal complex comprising at least a social contacting region of a Ras protein and at least a Son of sevenless (Sos) protein catalytic region fragment, that effectively diffracts X-rays. Ras and Sos form a tight complex. Sos does not impede the binding sites for the nucleotide base and the ribose of GTP or GDP and thus the Ras-Sos complex maintains a structure that permits nucleotide release and rebinding. The crystals are used for the nucleotide release and rebinding. The crystals are used for the three-dimensional coordinates of the complex to a resolution of more than 5.0 Angstrom. The crystals, or a dataset comprising the three-dimensional coordinates obtained from the crystals, is useful for of dentlifying an agent that stabilizes the Ras-Sos complex. The crystals are also useful for identifying agents that inhibit the formation of Ras-Sos complex. Ras and Sos fragments are useful for cordinates obtained from complex. Agents that stabilize treatment of cancer. The present sequence represents a yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY34584-Y35879 represent the proteins encoded by all,the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and
                      Novel crystals comprising a Ras-Son of sevenless complex, useful for screening drugs useful in cancer treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 21; Length 1048;
Pred. No. 17;
5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia pneumoniae protein not found in C. trachomatis.
                                                                                           Disclosure; Page 181-185; 224pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 1060; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY35210 standard; Protein; 212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1002 PNSNSNNKSQEKSRDDQTDE 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 PNTNKSEKAERKSHDTQTTQ 22
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97FR-0014673
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Best Local Similarity 45.v.
First Conservative
First Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sos-related protien.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-357842/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1048 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET
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21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY35210;
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  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer associated nucleic acid molecules (N) and proteins (P), where
the proteins are collectively known as colon cancer antigens. The colon
cancer antigens have cytostatic activity and can be used in gene
therapy and vaccine production. N and P may be used in the prevention,
diagnosis and treatment of diseases associated with inappropriate P
expression. For example, N and P may be used to treat disorders
associated with decreased expression by rectifying mutations or deletions
in a patient's genome that affect the activity of P by expressing
confidence in a patient's genome that affect the activity of P by expressing
confidence in a patient's genome that affect the activity of P by expressing
confidence in a patient of suppression by rectifying mutations or deletions
confidence in a patient of suppression by rectifying mutations of P.
Additionally, N may be used to produce the colon cancer-associated Ps,
confidence in the prevention of Ps,
confidence in the prevention, diagnosis
and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
cand AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                               Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kuriyan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a Son of sevenless (Sos) related protein.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of sevenless; Sos; crystal; Ras-Sos complex; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54; DB 22; Length 600;
Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boriack-Sjodin A, Margarit SM, Bar-Sagi D, Cole P,
                                                                                             Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                 Claim 11; Page 7370-7373; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY68823 standard; protein; 1048 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 GNPNKGKSEKKEKTPLRDESTQEHSE 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                           Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.8%;
46.2%;
                                              (HUMA-) HUMAN GENOME SCI INC.
99US-0163280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0119794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein coordinate data.
                                                                                           Ruben SM, Barash SC,
                                                                                                                                       WPI; 2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI 2000-182647/16.
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Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           600 AA;
                                                                                                                                                                N-PSDB; AAH34497
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03-NOV-1999;
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RESULT 12 AAY68823

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Gaps

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              disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or phasryngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY40584 *V35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                    Gaps
bronchitis and is thought to be a contributing factor in heart
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                              Length 212;
                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia pneumoniae transmembrane protein sequence.
                                                                                                                                                                                           Score 51; DB 20;
Pred. No. 8;
7; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                             AAY34934 standard; Protein; 584 AA
                                                                                                                                                                                                                                                                    26
                                                                                                                                                                                                                                                                                                       39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; neutralising epitope.
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30.8%;
                                                                                                                                                                                            Query Match 36.7%;
Best Local Similarity 38.1%;
Matches 8; Conservative 7
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97FR-0014673
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                                                                                                                                                                                                                                                                    6 NKSEKAERKSHDTQTTQEICE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-357842/30.
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                             212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 584 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-1999
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                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               AAY34934;
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                                                                                                                                                                                                                                                                                                                                                           RESULT 14
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The invention provides a protein which has a molecular weight of 58 kD and has antigenicity of nucleocapsid protein (NP) of canine distemper virus (CDV) belonging to Morbillivius genus of Paramyxovirus family. The protein can be used to prepare a reagent for the determination of anti-CDV NP antibody by immobilizing the above protein on a carrier or a membrane as the active component. The reagent can be used for diagnosis of CDV infection, judgement of effect of vaccine and judgement of inoculation period. The reagent can determine anti-CDV NP antibody contained in canine serum easily. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A protein having antigenicity of canine distemper virus nucleocapsid protein - useful in the diagnosis of canine distemper virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 523;
                                                                                                                                                                                                                                                                                                                                             protein; canine distemper virus; CDV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49.5;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: October 11, 2002, 20:37:37 Job time : 64 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 11-13; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the Morbillivirus antigenic protein.
292 GIPNSNTLERAEKEAEKQESREQLSE 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MORG ) MORINAGA MILK IND CO LTD.
                                                                                                                                                                                                                                                                                         Morbillivirus antigenic protein.
                                                                                                                                          AAY56856 standard; Protein; 523
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Morbillivirus; Paramyxovirus.
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ilarity 47.6%;
Conservative
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nes 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                 Morbillivirus sp.
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                                                                                                                                                                                                                                          10-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-1998;
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                                                                                                                                                                                         AAY56856;
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Gaps

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8;

; Score 50; DB 20; ; Pred. No. 36; 10; Mismatches 8

8; Conservative

Length 584;

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

拗 protein - protein search, using sw model

October 11, 2002, 20:36:38; Search time 33 Seconds (without alignments)
19.244 Million cell updates/sec Run on:

US-09-794-764-195 Perfect score:

139 1 GKPNTNKSEKAERKSHDTQTTQEICE 26 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

231628 segs, 24425594 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match | 0% Maximum Match | 100% Listing first | 45 summaries

Issued_Patents_AA:* Database :

1: /cgn2_6/ptddata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptddata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptddata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptddata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptddata/2/iaa/FCTUS_COMB.pep:*
6: /cgn2_6/ptddata/2/iaa/FCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

G	53,			38	39	36	39	ν,	7,	4	δ	13,	10,		17,		8,	1,	7	26,	4	26,	27,	7	12,	
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ΩΙ	US-08-845-258-53	-08-845-258-3	8-990-571-3	-08-723-142A-	-08-845-258-3	-08-990-571-3	-08-723-142A	-09-326	-08-841-349-	-08-841-349	9-185-160	3-185-160-1	-348-792	3-462-738-1	3-131-625B-1	395	3-691-814	9-185-160-	-24	3-463-587A-	3-463	08-923-854-2	I-US91	19-352-990-	-459-346	-08-889-419-1
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Length 1	275	. 4	4	445	32	32	32	1048	220	2154	259	734	343	343	123	123	534	731	752	461	461	461	461	546	588	588
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Score	139	m	m	m	63	63	63	54	47	47	46	46	44	44	43	43	43	43	43	42	42	42	42	42	42	42
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Appl Appl Appl Appl Appl Appl

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Sequence 12, Appl Sequence 6, Appl Sequence 6, Appli Sequence 13, Appl Sequence 11, Appl Sequence 13, Appl Sequence 51, Appl Sequence 51, Appl Sequence 52, Appl Sequence 7, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 6, Appli Sequence 1, Appli
PCT - US93 - 07189 - 12 US - 08 - 687 - 956 A - 23 US - 08 - 296 A - 23 US - 08 - 296 - 791 - 6 US - 08 - 789 - 464 A - 13 US - 08 - 686 C - 11 PCT - US95 - 1090 A - 53 PCT - US95 - 1090 A - 55 PCT - US95 - 1090 A - 55 US - 07 - 942 - 245 - 455 US - 08 - 712 - 948 - 2 US - 08 - 712 - 948 - 1 US - 08 - 712 - 948 - 1 US - 08 - 712 - 948 - 1 US - 08 - 741 - 134 - 6 US - 09 - 741 - 134 - 6 US - 08 - 741 - 134 - 6 US - 09 - 741 - 134 - 6
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0.000000000000000000000000000000000000
4444 11444 1171-1552 14444 1174-1174 14444 1444 1444 1444 14
00000000000000000000000000000000000000

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210121.426C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
Sequence 53, Application US/08845258 Patent No. 6183976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
REFERENCE/DOCKET NUMBER: 21012
RELECOMMUNICATION INFORMATION:
TELEFAX: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ), ORGANISM: Babesia Microti
US-08-845-258-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                              STREET: 6300 CCTTY: Seattle STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98104
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Gaps

0;

Length 275; Indels

Query Match 100.0%; Score 139; DB 4; Best Local Similarity 100.0%; Pred. No. 1.5e-13; Matches 26; Conservative 0; Mismatches 0;

26, Appl 27, Appl

App]

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GENERAL INFORMATION:
APPLICANT: Reed, Steven G. et al.
APPLICANT: Reed, Steven G. et al.
APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF INTHER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
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                                   COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
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COMPUTER: Elber COMPUTER:
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DATIG J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.426C1
TELECOMMULICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: Patentin Release #1.0, Version #1.30 APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
FILING DATE: 11-DEC-1997
CLASSIFICATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 139; DB 4;
Pred. No. 2.5e-13;
; Mismatches 0;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 GKPNTNKSEKAERKSHDTQTTQEICE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98104
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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Patent No. 6214971
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 445 amino acids
amino acid
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Best Local Similarity 100.
Matches 26; Conservative
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US-08-845-258-38
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                                                                                                                                                     Sequence 53, Application US/08990571
Patent No. 5214971
GENERAL INFORMATION:
GAPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
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APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Sleath, Pughton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 139; DB 4; Length 275; Best Local Similarity 100.0%; Pred. No. 1.5e-13; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                    STREET: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/990,571 FILING DATE: 11-DEC-1997 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DCOKET NUMBER: 210121.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)62-6031
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
                          218 GKPNTNKSEKAERKSHDTOTTOEICE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 GKPNTNKSEKAERKSHDTQTTQEICE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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Patent No. 6183976
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Babesia Microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
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US-08-845-258-38
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/note= "Residue can be either Gly or Asp"
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or Arg"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Residue can be either His or Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Residue can be either Lys
or Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Residue can be either Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Residue can be either or Gly"
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                                                                                ADDRESSEE: SEED AND BERRY STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)62-6031
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/845,258 FILING DATE: 24-APR-1997 CLASSIFICATION: 435
                                                                                                                                               CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 11
OTHER INFORMATION: /note
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NAME/KEY: Modified-site
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LOCATION: 7
OTHER INFORMATION: /note
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LOCATION: 18
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LOCATION: 5
OTHER INFORMATION: /note
OTHER INFORMATION: Or I]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 15
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
OTHER INFORMATION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
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LOCATION:
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Patent No. 6183976
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Bloghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul BAPLICANT: Sleath, Paul BAPLICANTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION NUMBER OF SEQUENCES: 49
CORRESPONDENCE SEED AND BERNY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                               Query Match 100.0%; Score 139; DB 4; Length 445; Best Local Similarity 100.0%; Pred. No. 2.5e-13; Matches 26; Conservative 0; Mismatches 0; Indels (
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MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: THE PC compatible
COMPUTER: THE PC compatible
COMPUTER: THE PC compatible
COMPUTER: THE PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,142A
FILING DATE: 01-0CT-1956
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DATIG 33
REGISTRATION NUMBER: 31, 392
REGISTRATION NUMBER: 31, 210121.426
TELEPHONE: (206) 622-6931
INFORMATION FOR SEQ ID NO: TELEFAX: (206) 682-6031
SEQUENCE CHARACTERISTICS:
LEMGTH: 445 mmino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                  182 GKPNTNKSEKAERKSHDTQTTQEICE 207
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                                                                                                                                                                                                     1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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: Sequence 38, Application US/08723142A
: Patent No. 6306396
: GENERAL INFORMATION:
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STATE: Washington
COUNTRY: ITCA
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US-08-723-142A-38
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FEATURE:
NAME/KEY: Modified-site
LOCATION: 27
OTHER INFORMATION: Or Ser"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 28
OTHER INFORMATION: /note="Residue can be either Cys
OTHER INFORMATION: /note="Residue can be either Asp
OTHER INFORMATION: or Glu"
FEATURE:
                                                                                                                                                                                                                                                                          LOCATION:
LOCATION:
LOCATION:
LOCATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
NAME/KEY:
MAME/KEY:
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LOCATION: 11
OTHER INFORMATION: /note= "Residue can be either Glu
OTHER INFORMATION: or Gly"
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                                                                                                                                                        OTHER INFORMATION: /note= "Residue can be either Gly OTHER INFORMATION: or Asp" ?FATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note= "Residue can be either Lys OTHER INFORMATION: or Asn"
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LOCATION: 26
COTCATION: 26
OTHER INFORMATION: /note="Residue can be either lle
OTHER INFORMATION: or Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 7
COTHER INFORMATION: /note= "Residue can be either Lys
OTHER INFORMATION: or Thr"
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OTHER INFORMATION: or Arg"
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OTHER INFORMATION: or Pro"
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or Ala"
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                         TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
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NAME/KEY: Modified-site
LOCATION: 15
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CTHER INFORMATION:
CTHER INFORMATION:
US-08-990-571-39
         STRANDEDNESS:
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Patent No. 6214971
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M
NUMBER OF SEQUENCES:
ADDRESSEE: SEED AND BERRY
ADDRESSEE: SEED AND BERRY
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Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
OTHER INFORMATION: /note= "Residue can be either Thr
OTHER INFORMATION: or Pro"
                                                                                       NAME/KEY: Modified-site
LOCATION: 26
OCHER INFORMATION: /note= "Residue can be either Ile
OTHER INFORMATION: or Thr"
                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /note= "Residue can be either Cys
OTHER INFORMATION: or Ser"
FEATURE:
NAME/KEY: Modified-site
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or Glu"
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or Ala"
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or His"
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 9810
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION UNMER: US/08/990,571
FILING DATE: 11-DEC-1997
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)62-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Best Local Similarity 63.6%;
Matches 14; Conservative
                                                                                                                                                                                                                                                   NAME/KEY: Modified-site LOCATION: 27
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OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-845-258-39
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either

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Sequence 5, Application US/09356952
Patent No. 6117663
GENERAL INFORMATION:
APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Boriack-Sodin, Dafna
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: HERROF
FILE REFERENCE: 600-1-228M
CURRENT APPLICATION NUMBER: US/09/356,952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.3%; Score 63; DB 4; Length 32; 63.6%; Pred. No. 0.004;
            /note= "Residue can be either Lys or Asn"
                                                                                                               /note= "Residue can be either Glu or Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Residue can be either Ile
or Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Residue can be either Cys
or Ser"
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or Glu"
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                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Residue can be either or Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Residue can be either or Ala"
                                                                                                                                                                                                                                                                                                                      /note= "Residue can be either or Tyr"
                                                                                                                                                                                                                   /note= "Residue can be or Arg"
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                                                                                                                                                                           NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: /note-
OTHER INFORMATION: or Arg
FEATURE:
                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
LOCATION: 18
OTHER INFORMATION: /note=
OTHER INFORMATION: or Tyr
FEATURE:
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LOCATION: 23
OTHER INFORMATION: /note-
OTHER INFORMATION: Or Pro
FEATURE:
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NAME/KEY: Modified-site
LOCATION: 28
OTHER INFORMATION: /note
OTHER INFORMATION: or Gl
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NAME/KEY: Modified-site
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                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Modified-site
LOCATION: 26
OTHER INFORMATION: /note
OTHER INFORMATION: or Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: Modified.
                                                                                                LOCATION: 14
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
Matches 14; Conservi
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US-09-356-952-5
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                                                            Gaps
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                                                                                                                                                                                                                                                                                             APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Raymond
TITLE OF INVENTION: COMPOINDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
CORRESPONDENCE: 49
CORRESPONDENCE: ADDRESS:
                Score 63; DB 4; Length 32;
Pred. No. 0.004;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /note= "Residue can be either Glu OTHER INFORMATION: or \text{Gl}\gamma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Residue can be either Pro
or lle"
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OTHER INFORMATION: /note= "Residue can be either Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /note= "Residue can be either Gly
OTHER INFORMATION: or Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER FORM:

MEDULUM TYPE: Floppy disk
MEDULUM TYPE: Floppy disk
COMPUTER: I'BM PC Compatible
COMPUTER: Platent PC Compatible
COMPUTER: Patent PC Compatible
CORERAT APPLICATION DATA:
APPLICATION NUMBER: US,08/723,142A
FILING DATE: 01-0CT-1946
CLASSIFICATION: 536
ATTORNEY/ACENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.426
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 39:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                  Sequence 39, Application US/08723142A
Patent No. 6306396
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
                                                                                                2 KPNTNKSEKAERKSHDTQTTÖE 23
                                                                                                                       4 KXNXNKSXXAXXKSXDTQTXQE 25
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              Query Match
Best Local Similarity 63.6\(\beta\);
Matches 14; Conservative
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NAME/KEY: Modified-site
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 5
OTHER INFORMATION:
OTHER INFORMATION:
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STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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RESULT 12
US-09-185-160-9
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Patent No. 595594
GENERAL INFORMATION:
APPLICANT: MISHRA, LOPA
TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT. . . .
FILE REFERENCE: XX/PO4470US0
CURRENT APPLICATION NUMBER: US/08/841,349B
CURRENT FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 18
SOGTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: MISHRA, LOPA
APPLICANT: MISHRA, LOPA
TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT.
FILE REFERENCE: XX/PO4470US0
CURRENT APPLICATION NUMBER: US/08/841,349B
CURRENT FILING DATE: 199-04-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                   Length 1048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 33.8%; Score 47; DB 2; Length 220; Best Local Similarity 37.5%; Pred. No. 9.8; Matches 9; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                   38.8%; Score 54; 45.0%; Pred. No.
CURRENT FILING DATE: 1999-07-19
EARLIER APPLICATION UNMBER: 60/093,631
EARLIER FILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 5
LENGTH: 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2092 PNTKVSEEAESQQWDTSKGDQVSQ 2115
                                                                                                                                    ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-356-952-5
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08841349B Patent No. 5955594
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                                                                                                                                                                                              Query Match
Best Local Similarity 45.vv
From 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus US-08-841-349-7
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GENERAL INFORMATION:

APPLICANT: ODELL, JOAN T.

APPLICANT: HARDER, PATRICIA A.

TITLE OF INVENTION: SOYBEAN HOMOLOG OF A SEED-SPECIFIC

TITLE OF INVENTION: TRANSCRIPTION ACTIVATOR FROM PHASEOLUS;

TITLE OF INVENTION: VULGARIS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DUPONT DE NEMOURS AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILLMINGTON

STATE: DELAMARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                            GENERAL INFORMATION:
APPLICANT: ODELL, JOAN T.
APPLICANT: HARDER, PATRICIA A.
TITLE OF INVENTION: SOYBEAN HOMOLOG OF A SEED-SPECIFIC
TITLE OF INVENTION: TRANSCRIPTION ACTIVATOR FROM PHASEOLUS
TITLE OF INVENTION: VULGARIS
NUMBER OF SEQUENCES: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DUPONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
FILING DATE:
CLASSOFT WICKOSOFT WINDOWS 9:
CURRENT APPLICATION DATA:
FILING DATE:
CLASSOFT WICKOSOFT WINDOWS 9:
CLASSOFT WINDOWS 9:
CLASSOFT
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/065,459
FILING DATE: NOVEMBER 12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MAJARIAN, WILLIAM R.
REFERENCE/DOCKET NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1096
TELECHONE: 302-992-4926
TELECHONE: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-185-160-13; Sequence 13, Application US/09185160; Patent No. 6252137
; Sequence 9, Application US/09185160
; Patent No. 6252137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 259 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 KPETKKAGKSQKNQHGTGT 230
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Best Local Similarity 42.1
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDAMAN
STREET: 1007, ...
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
7TP: 19898
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Sequence 10, Application US/08462738

Sequence 10. S977303

Patent No. S977303

GENERAL INFORMATION:
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                        ő
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0
                                                                                                                                                                                                                                       Score 44; DB 1; Length 343;
Pred. No. 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,738
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8;
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Pred. No. 47;
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                                                                                                                                                                                                                                                                                                     2; Mismatches
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FILING DATE: 05-JUN.
FILING DATE: 05-JUN.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAING, EGWID P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GB
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEPHONE: 415-852-9196
TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              31.78;
47.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 KSGPQEKKLHDALTDQDPC 311
                                                                                                                                                                                                                                                                                                                                                                                                                            293 KSGPQEKKLHDALTDQDPC 311
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amino acid
                                                                343 amino acids
INFORMATION FOR SEC ID NO:
                                                                                                                                                                                                                                                                           Best_Local Similarity 47.4 Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 47.4
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: California
COUNTY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
                            SEQUENCE CHARACTERISTICS
                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-348-792-10
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                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks B.
APPLICANT: Cocks 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/348,792
FILING DATE: 02-DEC-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ching, EGWIN P.
REGISTRATION NUMBER: 34,090
                                             MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/065,459
FILING DATE: NOVEMBER 12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1096
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
                                                                                                                                                                                                          APPLICATION NUMBER: US/09/185,160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-348-792-10; Sequence 10, Application US/08348792; Patent No. 5576423; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX(
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            687 KPETKKAGKSOKNOHGTGT 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KPNTNKSEKAERKSHDTQT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    734 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . MOLECULE TYPE: peptide US-09-185-160-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                         COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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